

SEQUENCE LISTING

<110> E. I. du Pont de Nemours and Company

<120> Plant Histidine Biosynthetic Enzymes

<130> BB1255

<140>

<141>

<150> 60/105,409

<151> 1998-10-23

<160> 22

<170> Microsoft Office 97

<210> 1

<211> 433

<212> DNA

<213> Zea mays

<220>

<221> unsure

<222> (432)

<400> 1

```

gccgcctcct cccagccacc gcgctgccgc tgtccagcgc tcctcggcca gctccccagc 60
gcgcagtcce agccgcccgc cagcgccccc cgcgcagtc tagccgccgc gcagccgccg 120
accagcgcac ctccggccag ctccctggcg tgcagctcct ccactagccg ccaagcacca 180
ggaccacgcc atggccgtct gtctcccaaa gtatgtgttt agcgatggca agatgaacat 240
tgaaaggctg acaaaacttg tcgagctggt tgggaaacag aggcttggtc tggaccttaa 300
gctgtcgaaa aaaggatggc aagatatact attgtaactg acaggtggca aaagttcagt 360
gatgtgtttg tggatgaacc ggcattagaa tatctcgtg cctttcgcag attagttttt 420
tggttcacgg gng                                     433

```

<210> 2

<211> 74

<212> PRT

<213> Zea mays

<400> 2

```

Gln Asp His Ala Met Ala Val Cys Leu Pro Lys Tyr Val Phe Ser Asp
 1              5              10              15

Gly Lys Met Asn Ile Glu Arg Leu Thr Lys Leu Val Glu Leu Val Gly
      20              25              30

Lys Gln Arg Leu Val Leu Asp Leu Lys Leu Ser Lys Lys Ala Arg Tyr
      35              40              45

Thr Ile Val Thr Asp Arg Trp Gln Lys Phe Ser Asp Val Phe Val Asp
      50              55              60

Glu Pro Ala Leu Glu Tyr Leu Ala Ala Phe
      65              70

```

<210> 3

<211> 490

<212> DNA
<213> Zea mays

<220>
<221> unsure
<222> (261)

<220>
<221> unsure
<222> (311)

<220>
<221> unsure
<222> (413)

<220>
<221> unsure
<222> (418)

<220>
<221> unsure
<222> (439)

<220>
<221> unsure
<222> (442)

<220>
<221> unsure
<222> (488)

<400> 3
gctagtatgt gaattgcagg ttaggaattg atgaggaact tgtggaacta ttggggcact 60
attcaccaat cccagtcact tatgctgggg gtgtgtcaac aatggacgac ctagagagga 120
taaagaaaagc aggcaaaagt cgggtagatg taacaattgg gagtgtctta gatataattg 180
gaggagattt gccttacaaa gatgttgtcc tttggcacag gaagcaaagt atggttgggc 240
aagtgtgaag aaacacaagg nattgatcag tattaccagt tcatttgatt caagcttctg 300
cacaaaagtat nttttctgaa catttttgtt caaataattc aagttaggct atctccaaca 360
agatcctcct atctcatccc cctattttcaa acctattttg cgtcccctat ttntacanct 420
acactgggag acagtcctnc antgatggtt atctcaaadc tgggggagca atgaccttgc 480
tttggggntt 490

<210> 4
<211> 76
<212> PRT
<213> Zea mays

<400> 4
Arg Leu Gly Ile Asp Glu Glu Leu Val Glu Leu Leu Gly His Tyr Ser
1 5 10 15
Pro Ile Pro Val Thr Tyr Ala Gly Gly Val Ser Thr Met Asp Asp Leu
20 25 30
Glu Arg Ile Lys Lys Ala Gly Lys Ser Arg Val Asp Val Thr Ile Gly
35 40 45
Ser Ala Leu Asp Ile Phe Gly Gly Asp Leu Pro Tyr Lys Asp Val Val
50 55 60

Leu Trp His Arg Lys Gln Ser Met Val Gly Gln Val
 65 70 75

<210> 5
 <211> 466
 <212> DNA
 <213> Zea mays

<400> 5
 ggggttcgccc tgcgcgccgc gctacctcgc tccggctccc agctcgctccg gtccagctca 60
 ctgcggtcgc cgaccatctc cgtccacctc atccctccgg caagcagttg ctaaactcat 120
 ccagggtcag atcagcagct cttgccttat cccgctggct ggccgcagca ccggtggtgt 180
 ggtggaggat ggcacgaaa tacgtggcca ggtaccgtc tccatggtgg gcgccacaac 240
 gtcgtttggt tggttcatgg gtttccgtct gtcggtgaaa atgcggtgca ttgggaggac 300
 ggatgttgtg tgcgctgctg ttagcttcag accatgcac gacattcaca aggggaaagt 360
 taagcagatt gttggttcta ctcttcggga ttcattccaat gatggcatgg aacttgtgac 420
 aaactttgaa tcagacaaat ctctgcaga atttgcaaaa tcatat 466

<210> 6
 <211> 81
 <212> PRT
 <213> Zea mays

<400> 6
 Met Val Gly Ala Thr Thr Ser Phe Gly Trp Phe Met Gly Phe Arg Leu
 1 5 10 15

Leu Gly Lys Met Arg Cys Ile Gly Arg Thr Asp Val Val Cys Ala Ala
 20 25 30

Val Ser Phe Arg Pro Cys Ile Asp Ile His Lys Gly Lys Val Lys Gln
 35 40 45

Ile Val Gly Ser Thr Leu Arg Asp Ser Ser Asn Asp Gly Met Glu Leu
 50 55 60

Val Thr Asn Phe Glu Ser Asp Lys Ser Pro Ala Glu Phe Ala Lys Ser
 65 70 75 80

Tyr

<210> 7
 <211> 566
 <212> DNA
 <213> Zea mays

<220>
 <221> unsure
 <222> (326)

<220>
 <221> unsure
 <222> (340)

<220>
 <221> unsure
 <222> (383)

<220>
 <221> unsure
 <222> (398)

<220>
 <221> unsure
 <222> (418)

<220>
 <221> unsure
 <222> (437)

<220>
 <221> unsure
 <222> (443)..(444)

<220>
 <221> unsure
 <222> (485)

<220>
 <221> unsure
 <222> (488)

<220>
 <221> unsure
 <222> (516)

<220>
 <221> unsure
 <222> (522)

<220>
 <221> unsure
 <222> (539)

<220>
 <221> unsure
 <222> (551)

<400> 7
 cgtgctggac ctcagttgtc gaaaaaagga tggccgatat accattgtaa ctgacaggtg 60
 gcaaaaagtgc agtgatgtgt ttgtggatga accaacatta gaatatctcg ctgcctttgc 120
 agatgagttt ttggttcagtg gtgttgatgt ggagggc aaa aggttaggaa ttgatgagga 180
 acttgtggaa ctattggggc actattcacc aatcccagtc acttatgctg ggggtgtgtc 240
 aacaatggac gacctagaga ggataaagaa agcaggcaaa agtcgggtag atgtaacaat 300
 tgggagtgct ctagatataa ttggangaga ttgccttacn aagatgttgt ccttggcacc 360
 agggagccaa gtaatggttg ggncaagtgt gaagaacncc aggggaattaa tccagtanta 420
 cccagttcca tttgatnaaa ccnctggac caaaagataa tttccccgaa ccaatttttg 480
 gtccnaanaa atccaggtaa ggggaatttc ccaaanaaag anccccctaa cccaaccnc 540
 cccaatttcc naaaaccaaa attttc 566

<210> 8
 <211> 108
 <212> PRT
 <213> Zea mays

<400> 8
 Val Leu Asp Leu Ser Cys Arg Lys Lys Asp Gly Arg Tyr Thr Ile Val
 1 5 10 15

Thr Asp Arg Trp Gln Lys Phe Ser Asp Val Phe Val Asp Glu Pro Thr
20 25 30

Leu Glu Tyr Leu Ala Ala Phe Ala Asp Glu Phe Leu Val His Gly Val
35 40 45

Asp Val Glu Gly Lys Arg Leu Gly Ile Asp Glu Glu Leu Val Glu Leu
50 55 60

Leu Gly His Tyr Ser Pro Ile Pro Val Thr Tyr Ala Gly Gly Val Ser
65 70 75 80

Thr Met Asp Asp Leu Glu Arg Ile Lys Lys Ala Gly Lys Ser Arg Val
85 90 95

Asp Val Thr Ile Gly Ser Ala Leu Asp Ile Ile Gly
100 105

<210> 9

<211> 397

<212> DNA

<213> Zea mays

<400> 9

cacaaggagg aagttaagca gattgttggt tctactcttc gggattcatc caatgatggc 60
atggaacttg tgacaaactt tgaatcagac aaatctcctg cagaatttgc aaaatcatat 120
aaagaagatg aacttcttgg aggacatggt ataatgcttg gctcagatcc tgcaagccag 180
gctgctgcac tcgaggcact acatgcatat cctggtggct tgcaagttgg aggtggaata 240
aatttgcaga atgcaatgtc ttaccttaat gaaggggcca gtcattgtgat agtgacctct 300
tatgtgttta gcgatggcaa gatgaacatt gaaaggctga caaaacttgt cgagctgggt 360
gggaaacaga gcttgtgctg gaccttagct gtcgaaa 397

<210> 10

<211> 130

<212> PRT

<213> Zea mays

<400> 10

His Lys Gly Lys Val Lys Gln Ile Val Gly Ser Thr Leu Arg Asp Ser
1 5 10 15

Ser Asn Asp Gly Met Glu Leu Val Thr Asn Phe Glu Ser Asp Lys Ser
20 25 30

Pro Ala Glu Phe Ala Lys Ser Tyr Lys Glu Asp Glu Leu Gly Gly
35 40 45

His Val Ile Met Leu Gly Ser Asp Pro Ala Ser Gln Ala Ala Ala Leu
50 55 60

Glu Ala Leu His Ala Tyr Pro Gly Gly Leu Gln Val Gly Gly Gly Ile
65 70 75 80

Asn Leu Gln Asn Ala Met Ser Tyr Leu Asn Glu Gly Ala Ser His Val
85 90 95

Ile Val Thr Ser Tyr Val Phe Ser Asp Gly Lys Met Asn Ile Glu Arg
100 105 110

Leu Thr Lys Leu Val Glu Leu Val Gly Lys Gln Ser Leu Cys Trp Thr
 115 120 125

Leu Ala
 130

<210> 11
 <211> 423
 <212> DNA
 <213> Zea mays

<220>
 <221> unsure
 <222> (1)

<220>
 <221> unsure
 <222> (4)

<220>
 <221> unsure
 <222> (28)

<220>
 <221> unsure
 <222> (75)

<220>
 <221> unsure
 <222> (90)

<220>
 <221> unsure
 <222> (295)

<220>
 <221> unsure
 <222> (373)

<220>
 <221> unsure
 <222> (377)

<220>
 <221> unsure
 <222> (386)

<220>
 <221> unsure
 <222> (394) .. (395)

<400> 11
 ngcnttgctg ttagcttcag accatgcntt gacattcaca agggaaaagt taaacagatt 60
 gttggctcta ctctncggga tttagcaaan gatagcatgg aacttgtgac aaactttgaa 120
 tcagacaaat ctctgcaga atttgctaaa tttataaag cagatgaact tctaggagga 180
 catgttataa tgcttggcgc aaatccttca agccaggctg ctgcactgga ggcactacgt 240
 gcataatcctg gtgggtttgca agttggaggt gggataaatt tggagaatgc aatgncttac 300
 cttaatgaag gggccagaca tgtgatagtg acctcttatg tggttaggga tggcaagatg 360
 aacactgaaa ggntaanaaa acttgncgag ctgnntggga aacagaggct tcgtgctgga 420
 cct 423

<210> 12
 <211> 135
 <212> PRT
 <213> Zea mays

<220>
 <221> UNSURE
 <222> (8)

<220>
 <221> UNSURE
 <222> (28)

<220>
 <221> UNSURE
 <222> (97)

<220>
 <221> UNSURE
 <222> (123)..(124)

<220>
 <221> UNSURE
 <222> (127)

<220>
 <221> UNSURE
 <222> (130)

<400> 12
 Ala Val Ser Phe Arg Pro Cys Xaa Asp Ile His Lys Gly Lys Val Lys
 1 5 10 15
 Gln Ile Val Gly Ser Thr Leu Arg Asp Leu Ala Xaa Asp Ser Met Glu
 20 25 30
 Leu Val Thr Asn Phe Glu Ser Asp Lys Ser Pro Ala Glu Phe Ala Lys
 35 40 45
 Phe Tyr Lys Ala Asp Glu Leu Leu Gly Gly His Val Ile Met Leu Gly
 50 55 60
 Ala Asn Pro Ser Ser Gln Ala Ala Ala Leu Glu Ala Leu Arg Ala Tyr
 65 70 75 80
 Pro Gly Gly Leu Gln Val Gly Gly Gly Ile Asn Leu Glu Asn Ala Met
 85 90 95
 Xaa Tyr Leu Asn Glu Gly Ala Arg His Val Ile Val Thr Ser Tyr Val
 100 105 110
 Val Arg Asp Gly Lys Met Asn Thr Glu Arg Xaa Xaa Lys Leu Xaa Glu
 115 120 125
 Leu Xaa Gly Lys Gln Arg Leu
 130 135

<210> 13
 <211> 535

<212> DNA
<213> Zea mays

<220>
<221> unsure
<222> (442)

<220>
<221> unsure
<222> (459)

<220>
<221> unsure
<222> (474)

<220>
<221> unsure
<222> (498)

<220>
<221> unsure
<222> (519)

<400> 13
gtgacaaact ttgaatcaga caaatctcct gcagaatttg caaaatcata taaagaagat 60
gaacttcttg gaggacatgt tataatgctt ggctcagatc ctgcaagcca ggctgctgca 120
ctcgaggcac tacatgcata tcctggtggc ttgcaagttg gaggtggaat aaattttgcag 180
aatgcaatgt cttaccttag ctgtcgaaaa aaggatggca gatatactat tgtaactgac 240
aggtggcaga agttcagtga tgtgtttgtg gatgaaccgg cattaggata tctcgctgcc 300
ttcgcagatg agtttttggg tcatggtgtt gatgtggagg gcaaaaagggt agggattgat 360
gaggaacttg tggaactatt ggggcatcat tcaccaatcc cagtaactta tgctgggggt 420
gtgtcaacaa tggatgacct anagaggata aagaagcang caaaagtcga gtanatgtaa 480
ctgttgggag tgctctanat atatttggag gagaattanc ctacaaagaa tgttg 535

<210> 14
<211> 177
<212> PRT
<213> Zea mays

<220>
<221> UNSURE
<222> (148)

<220>
<221> UNSURE
<222> (152)

<220>
<221> UNSURE
<222> (154)

<220>
<221> UNSURE
<222> (159)

<220>
<221> UNSURE
<222> (167)

<220>

<221> UNSURE

<222> (174)

<400> 14

Val Thr Asn Phe Glu Ser Asp Lys Ser Pro Ala Glu Phe Ala Lys Ser
1 5 10 15

Tyr Lys Glu Asp Glu Leu Leu Gly Gly His Val Ile Met Leu Gly Ser
20 25 30

Asp Pro Ala Ser Gln Ala Ala Ala Leu Glu Ala Leu His Ala Tyr Pro
35 40 45

Gly Gly Leu Gln Val Gly Gly Gly Ile Asn Leu Gln Asn Ala Met Ser
50 55 60

Tyr Leu Ser Cys Arg Lys Lys Asp Gly Arg Tyr Thr Ile Val Thr Asp
65 70 75 80

Arg Trp Gln Lys Phe Ser Asp Val Phe Val Asp Glu Pro Ala Leu Gly
85 90 95

Tyr Leu Ala Ala Phe Ala Asp Glu Phe Leu Val His Gly Val Asp Val
100 105 110

Glu Gly Lys Arg Leu Gly Ile Asp Glu Glu Leu Val Glu Leu Leu Gly
115 120 125

His His Ser Pro Ile Pro Val Thr Tyr Ala Gly Gly Val Ser Thr Met
130 135 140

Asp Asp Leu Xaa Arg Ile Lys Xaa Ala Xaa Lys Ser Arg Val Xaa Val
145 150 155 160

Thr Val Gly Ser Ala Leu Xaa Ile Phe Gly Gly Glu Leu Xaa Tyr Lys
165 170 175

Glu

<210> 15

<211> 854

<212> DNA

<213> *Oryza sativa*

<400> 15

ctacaatgga tgacctagag aggataaaaa gagcaggcaa cagtcgagtt gatgttacgg 60
ttgggagtg ccttgatata ttcgaggag atttgcccta caaggacgtc gttctttggc 120
acaaggaaca aaatatggtt agccaacat gatatatcag aggtataatg cttaacctgt 180
tccatcagct cgattgttat gcacagacct ccagggtcta gaagtaatgc taatgcattt 240
tctcaagtgt tgtactgcca ataattcgat gggcttcttg tggataagt tcaagctgaa 300
gggttcgatt ttgttcggat ctggaactag gctttacatt gaggactggc cgagctgtt 360
atcaagcgac tgcactatat gtttttgaga ttaaaacact gttaacatga tatgtaagca 420
catctactga gttagcccgt ctgatggtga aacataatgg gggcctccac tagtccacag 480
ctcattaatc atactcaaca tttggcgtac caagctgcag tggttacagt gtgttttctt 540
tggaagtggg ccgagggtt tatgcccac ttaaaatgtg gtcatttccc caatttcctg 600
caggtcatgt gaaatcccta ctgcagtact cctatgtgtg ccaagcatgc caatgtggcc 660
atgtggcctg tgggtctatt ggcgacgttt ggctgtggag tactgctcag taatggatta 720
agtaaaacat ctcaaagcac catttgcaac ttctcagcag ttcataatgc aagagctgat 780

ttgtttggaa ctattaatgc atattgttgg tcttgtgatt gtactagtat tttcacaaaa 840
 aaaaaaaaaa aaaa 854

<210> 16
 <211> 49
 <212> PRT
 <213> Oryza sativa

<400> 16
 Thr Met Asp Asp Leu Glu Arg Ile Lys Arg Ala Gly Asn Ser Arg Val
 1 5 10 15
 Asp Val Thr Val Gly Ser Ala Leu Asp Ile Phe Gly Gly Asp Leu Pro
 20 25 30
 Tyr Lys Asp Val Val Leu Trp His Lys Glu Gln Asn Met Val Ser Gln
 35 40 45

Pro

<210> 17
 <211> 487
 <212> DNA
 <213> Glycine max

<220>
 <221> unsure
 <222> (473)

<220>
 <221> unsure
 <222> (477)

<220>
 <221> unsure
 <222> (481)

<400> 17
 ttctgttggt gtctcogttc attacatcgt agctccgatc accgagaatg cgtagtctcg 60
 ctgcacctca ttccttcogg gttttcgtca actcgcccat ctttcgcccc attagcttc 120
 cttttctcac tctcaaccct ctctcttcac cttccagaag atctccaagc ttccggtcaa 180
 tgcgcccgttc aattccgccc ctgcatcgac atccacaagg ggaaagtga gcaaattgtg 240
 gggtcgaccc ttcaagactt gaaaggggtt gacggttcgg atcccgtcac caatttcgag 300
 tcctgataag tcggctgctg agtatgccgc gctttacaaa caagatggac tcaactgggtg 360
 tcatgtcatc atgctcggag ccgacccttt gagcaaagct tctgcccttg aaagcattac 420
 acgccttata ctggcggggt tggaaagtcg ggggggggaa aaaaatttct gancaanttg 480
 ntttggtg 487

<210> 18
 <211> 108
 <212> PRT
 <213> Glycine max

<220>
 <221> UNSURE
 <222> (47)

<220>

<221> UNSURE

<222> (59)

<220>

<221> UNSURE

<222> (97)..(98)

<400> 18

Ser Leu Ser Thr Leu Ser Leu His Leu Pro Glu Asp Leu Gln Ala Ser
 1 5 10 15

Val Gln Cys Ala Val Gln Phe Arg Pro Cys Ile Asp Ile His Lys Gly
 20 25 30

Lys Val Lys Gln Ile Val Gly Ser Thr Leu Gln Asp Leu Lys Xaa Asp
 35 40 45

Gly Ser Asp Pro Val Thr Asn Phe Glu Ser Xaa Lys Ser Ala Ala Glu
 50 55 60

Tyr Ala Ala Leu Tyr Lys Gln Asp Gly Leu Thr Gly Gly His Val Ile
 65 70 75 80

Met Leu Gly Ala Asp Pro Leu Ser Lys Ala Ser Ala Leu Glu Ser Ile
 85 90 95

Xaa Xaa Tyr Pro Gly Gly Phe Gly Lys Ser Gly Gly
 100 105

<210> 19

<211> 981

<212> DNA

<213> Glycine max

<400> 19

gcaccagcag aaggtcaaca acgcatttcg cccattatt ttgattcttt cttctctttc 60
 ctttgaagtt acttgacata gagttttgtt cgtggacatc ttcccagcac aaactttggt 120
 gtcgagaaat tcctcataat gacgaaattc cgaccctgta tagacctgca ttccgggtcag 180
 gtgaagcaga ttgtaggtgg tacattgaca actgcttcct ctgatttgaa aaccaactat 240
 gtctcgaaat taccagctgg tcatttcgca aaactctaca aggagaatgg tcttaccggt 300
 gctcatgtca ttatgcttgg acctggaaat gaagaggcag ctaaagaagc cgtaggagag 360
 tggaaaaatg gtcttcaggt cggaggtggt attacgaatg aaaatgctaa gcaatggatt 420
 gattggggtg ctgagaggta ggtcattatt acttcttttc tatttcccaa tgggaagtgc 480
 tcccaagaac gattggattc cgtattggaa gctcttggtg gtgataaaga aaaacttgtc 540
 attgatctga gttgtcgaag gagagatgat acttggtttg tggctatgaa caaatggcag 600
 accatcacag atatggaggt aaatgcggca tctatcaaat ccttagagcc atattgctct 660
 gaattcttaa ttcattgcagc ggataacgaa ggcttgcaaa agggatcga tgaacaactt 720
 gtcgagaaat tggcacaatg gtgtagtatt ccagtcactt atgctggtgg cgggagaaac 780
 cttcaagatc ttgattatgt caagaaactg agtgggtggaa aagttgacct tacgattgga 840
 agtgctctag atgttttcgg aggttctgga gtcacatttg atgaatgtgt acaatggaac 900
 cagaggcaag ttgcttcttc ataaaatgca taaatgcaaa atggggcgct ccagtatctc 960
 gttaaaaaaa aaaaaaaaaa a 981

<210> 20

<211> 280

<212> PRT

<213> Glycine max

<220>

<221> UNSURE

<222> (120)

<400> 20

Ser Phe Val Arg Gly His Leu Pro Ser Thr Asn Phe Gly Val Glu Lys
 1 5 10 15

Phe Leu Ile Met Thr Lys Phe Arg Pro Cys Ile Asp Leu His Ser Gly
 20 25 30

Gln Val Lys Gln Ile Val Gly Gly Thr Leu Thr Thr Ala Ser Ser Asp
 35 40 45

Leu Lys Thr Asn Tyr Val Ser Lys Leu Pro Ala Gly His Phe Ala Lys
 50 55 60

Leu Tyr Lys Glu Asn Gly Leu Thr Gly Ala His Val Ile Met Leu Gly
 65 70 75 80

Pro Gly Asn Glu Glu Ala Ala Lys Glu Ala Val Gly Glu Trp Lys Asn
 85 90 95

Gly Leu Gln Val Gly Gly Gly Ile Thr Asn Glu Asn Ala Lys Gln Trp
 100 105 110

Ile Asp Trp Gly Ala Glu Arg Xaa Val Ile Ile Thr Ser Phe Leu Phe
 115 120 125

Pro Asn Gly Lys Phe Ser Gln Glu Arg Leu Asp Ser Val Leu Glu Ala
 130 135 140

Leu Gly Gly Asp Lys Glu Lys Leu Val Ile Asp Leu Ser Cys Arg Arg
 145 150 155 160

Arg Asp Asp Thr Trp Phe Val Ala Met Asn Lys Trp Gln Thr Ile Thr
 165 170 175

Asp Met Glu Val Asn Ala Ala Ser Ile Lys Ser Leu Glu Pro Tyr Cys
 180 185 190

Ser Glu Phe Leu Ile His Ala Ala Asp Asn Glu Gly Leu Gln Lys Gly
 195 200 205

Ile Asp Glu Gln Leu Val Glu Lys Leu Ala Gln Trp Cys Ser Ile Pro
 210 215 220

Val Thr Tyr Ala Gly Gly Gly Arg Asn Leu Gln Asp Leu Asp Tyr Val
 225 230 235 240

Lys Lys Leu Ser Gly Gly Lys Val Asp Leu Thr Ile Gly Ser Ala Leu
 245 250 255

Asp Val Phe Gly Gly Ser Gly Val Thr Phe Asp Glu Cys Val Gln Trp
 260 265 270

Asn Gln Arg Gln Val Ala Ser Ser
 275 280

<210> 21
 <211> 1210
 <212> DNA
 <213> Triticum aestivum

<400> 21
 tcgccgttgg aactcgacgg aaaaacccta ccccgccgtc gcccacatcgt cgaacttccc 60
 gatggcgctcg agatgcgcgg cgaggcttcc acaccgcggc tgcgcggcgc cgcaccacgg 120
 ttgggcgagc tcgcgggtct cggcacgccc ggcgcaatcc ggcgcgctcaa gagggcggtgc 180
 cgctcgtgtgc gccgtcagct tcaggccatg tatcgacatt cacaagggga aagttaaaca 240
 gattgttggc tctactctcc gggatgcac ggacgatggc acggcactag tgacaaactt 300
 tgaatcagac aagtctccag cagaatttgc aaatatttat aaagaggatg gacttggttg 360
 tggacatgta ataatgcttg gcggagaccc tgcaagccgt tctgctgccc tggaagcact 420
 acatgcatat cctggtggtt tgcaagttgg aggtggaata aatttggaga atgcaatgtc 480
 ataccttaat gaaggagcaa gtcacgtgat tgtaacttct tatgtgttta gtgatggcaa 540
 aatgaacatt gaaaggctga cgcaacttgt cgagcttggt gggaaagaaa ggcttatttt 600
 ggacctgagt tgtcgaaaaa aggatggcag atatgccatt gtgactgaca gatggcagaa 660
 gttcagtgat gtctttgttg atgggccaac attagaacgt cttgctgcat atgcagatga 720
 gtttttgggt catggagttg atgtggaggg caaaagggtta ggaattgatg aggaactcgt 780
 ggagctactg ggaagtcatt cacctatccc gacaacatac gccggggggc tgtaagcact 840
 ggacgacctg gagaggatca agaaagcagg caagagccga gtcgatgtca ctgtcgggag 900
 cgccctagac atatttgggg gagatttggc gtacgatgat gttgtccgtt ggcacaagga 960
 gcaaaacctg gttagcaaac ggtgaagaaa tcagatgtac actttgacca atacggtcag 1020
 gttatagggc ttgtttgctg gacagtgtgg cgctgacagt ttgtgtcttg tgtgacttcc 1080
 aaagctgaag cagaggtgtc aacctcgggt tggtagagga ccactcggta ttcagatact 1140
 gtactttaca ttctgtttgt attgtaatga taataaagag aggctggact gcaaaaaaaaa 1200
 aaaaaaaaaa 1210

<210> 22
 <211> 327
 <212> PRT
 <213> Triticum aestivum

<400> 22
 Arg Arg Trp Asn Ser Thr Glu Lys Pro Tyr Pro Ala Val Ala Pro Ser
 1 5 10 15
 Ser Asn Phe Pro Met Ala Ser Arg Cys Ala Ala Arg Leu Pro His Pro
 20 25 30
 Pro Cys Ala Ala Pro His His Gly Trp Ala Ser Ser Arg Val Ser Ala
 35 40 45
 Arg Pro Ala Gln Ser Gly Ala Ser Arg Gly Arg Ala Val Val Cys Ala
 50 55 60
 Val Ser Phe Arg Pro Cys Ile Asp Ile His Lys Gly Lys Val Lys Gln
 65 70 75 80
 Ile Val Gly Ser Thr Leu Arg Asp Ala Ser Asp Asp Gly Thr Ala Leu
 85 90 95
 Val Thr Asn Phe Glu Ser Asp Lys Ser Pro Ala Glu Phe Ala Asn Ile
 100 105 110
 Tyr Lys Glu Asp Gly Leu Val Gly Gly His Val Ile Met Leu Gly Gly
 115 120 125
 Asp Pro Ala Ser Arg Ser Ala Ala Leu Glu Ala Leu His Ala Tyr Pro
 130 135 140

Gly Gly Leu Gln Val Gly Gly Gly Ile Asn Leu Glu Asn Ala Met Ser
 145 150 155 160
 Tyr Leu Asn Glu Gly Ala Ser His Val Ile Val Thr Ser Tyr Val Phe
 165 170 175
 Ser Asp Gly Lys Met Asn Ile Glu Arg Leu Thr Gln Leu Val Glu Leu
 180 185 190
 Val Gly Lys Glu Arg Leu Ile Leu Asp Leu Ser Cys Arg Lys Lys Asp
 195 200 205
 Gly Arg Tyr Ala Ile Val Thr Asp Arg Trp Gln Lys Phe Ser Asp Val
 210 215 220
 Phe Val Asp Gly Pro Thr Leu Glu Arg Leu Ala Ala Tyr Ala Asp Glu
 225 230 235 240
 Phe Leu Val His Gly Val Asp Val Glu Gly Lys Arg Leu Gly Ile Asp
 245 250 255
 Glu Glu Leu Val Glu Leu Leu Gly Ser His Ser Pro Ile Pro Thr Thr
 260 265 270
 Tyr Ala Gly Gly Val Ser Thr Met Asp Asp Leu Glu Arg Ile Lys Lys
 275 280 285
 Ala Gly Lys Ser Arg Val Asp Val Thr Val Gly Ser Ala Leu Asp Ile
 290 295 300
 Phe Gly Gly Asp Leu Pro Tyr Asp Asp Val Val Arg Trp His Lys Glu
 305 310 315 320
 Gln Asn Leu Val Ser Lys Arg
 325